



**Full Length Research Article**

**STUDIES ON GENETIC DIVERGENCE IN INTRAHIRSUTUM HYBRIDS OF EARLY SEGREGATING GENERATION (F<sub>3</sub>) IN UPLAND COTTON (*GOSSYPIUMHIRSUTUM* L.)**

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**ARTICLE INFO**

**Article History:**

Received 12<sup>th</sup> December, 2013  
Received in revised form  
18<sup>th</sup> January, 2014  
Accepted 26<sup>th</sup> February, 2014  
Published online 25<sup>th</sup> March, 2014

**Key words:**

Cluster,  
Genetic divergence,  
Inter cluster,  
Intra cluster,  
Intrahirsutumcotton

**ABSTRACT**

Genetic Divergence in 86 intrahirsutum lines in early segregating generation genotypes was studied for 15 yield attributes and quality characters. The pattern of grouping of genotypes revealed that the genetic divergence was not fully related to the geographical diversity. The inter cluster distances were found to be greater than intra cluster distances, revealing considerable amount of genetic diversity among the genotypes studied. Inter cluster distances, cluster for all the characters studied and cluster wise performance of all the genotypes suggested that the genotypes selected for improvement of yield and quality components were divergent in terms of characters studied. The hybridization program with the selected genotypes by considering inter cluster distances may produce high magnitude of heterosis or desirable segregants, which would be meaningful for improvement in yield and quality attributes of cotton

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**INTRODUCTION**

Cotton is the most important fibre crop and back bone of textile industry of India. It alone accounts for 70 per cent of total fibre consumption in textile sector with approximately of 38 per cent of the country's export. India ranks first in area under cotton cultivation. Among four linted cotton species, upland cotton (*Gossypiumhirsutum* L.) is apredominant species of cotton in the world as well as of India. By virtue of its wider adaptability, higher yield and good fibre quality, it gradually replaced Asiatic diploid cottons and was grown under irrigated as well as rain fed conditions. Varieties and hybrids of *G.hirsutum* occupy about 75 per cent area and 85 per cent cotton production. However, Indian cotton productivity is quite low (403kg lint/ha) as against the worlds productivity (600 kg lint/ha). Genetic diversity plays a key role in analyzing the general distance among the genotypes selected as parent. Within a certain limit, hybridization of more diverged parents is expected to enhance the level of heterosis in hybrids and generate wide range of variability in segregating generations (Joshi and Dhavan, 1966). Therefore, the present investigation was undertaken to study the nature and magnitude of genetic divergence in 86 cotton genotypes under rainfed situation.

**MATERIALS AND METHODS**

The study was conducted in the Instructional Farm, Agriculture Research Station, Hebballi, under University of Agriculture Sciences, Dharwad. 86 genotypes, obtained from intrahirsutum crosses were planted in augmented design. Uniform spacing of 90X20 cm and all standard manurial and cultural treatments were adopted. In each line, 10 plants were randomly selected and observations were recorded for 15 characters viz., plant height, number of monopodia per plant, number of sympodia per plant, sympodial length at 50 per cent per plant, number of nodes per plant, inter boll distance, stem diameter, number of seeds per boll, seed index, lint index ginning outturn, halo length, boll weight, number of bolls per plant, seed cotton yield per plant. The genetic divergence was worked out by using Mahalonobis D<sup>2</sup> statistic as described by Rao (1952). On the basis of D<sup>2</sup> values, investigated genotypes were grouped into different clusters by employing Toscher method as outlined by Rao (1952).

**RESULTS AND DISCUSSION**

The analysis of variance indicated significant differences among all the genotypes for all the characters and specified of considerable genetic diversity among genotypes. Hence, further analysis was carried out for magnitude of D<sup>2</sup> values for

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all the characters and all the genotypes were grouped into nine clusters (Table 1). Creation of variability and selection within, leading to diverse genotypes is the common protocol a conventional plant breeder follows. Genetic relationship among genotypes thus generated can be measured by similarity or dissimilarity of any number of quantitative characters assuming that the differences between characters of genotypes ultimately reflect in the divergence of genotypes. In heterosis breeding programs the diversity of parents is always emphasized upon. More diverse the parents within a reasonable range, better the chances of improving economic traits under consideration in the resulting offspring. Based on D<sup>2</sup> values, the set of 86 single cross derived lines were grouped into nine clusters indicating the presence of appreciable amount of genetic diversity among the genotypes under study. The maximum number of genotypes (53) was grouped into Cluster I, followed by Cluster II with 19 genotypes and Cluster III with 8 genotypes. Remaining six clusters (IV, V, VI, VII, VIII, IX) were all solitary, each containing a single genotype. The intra-cluster D<sup>2</sup> values ranged from 19.37 to 21.07. The average intra-cluster distance between the members of Cluster III was maximum followed by Clusters II and I suggesting that genotypes in Cluster III were relatively more diverse than genotypes in the other clusters.

According to theory, the maximum amount of heterosis is expected in cross combinations involving the parents belonging to the most divergent clusters. In the present study, inter-cluster D<sup>2</sup> values ranged widely with minimum value of 13.71 and maximum value of 64.95. Cluster V and IX were strikingly diverse from the rest of the clusters. The divergence between these two clusters was high as evident from their high inter-cluster distance. Crossing between the members of these two clusters may generate wider variability and is expected to throw high yielding transgressive segregants in a hybridization and selection programme. The minimum inter-cluster D<sup>2</sup> value (13.71) was observed between clusters VI and VII indicating a closer relationship between genotypes of these two clusters. Based on these findings, hybridization between progenies of diverse F<sub>3</sub> lines for the purpose of extracting superior segregants is highly advised as these lines are in early segregation stage and may throw out a myriad of variations.

### Contribution of characters towards divergence

Among the sixteen characters studied, the most important character contributing to the divergence was plant height, followed by number of nodes, sympodial length at 50 per cent plant height, number of seeds per boll, monopodia, stem girth, bolls, sympodial angle, number of bolls, seed index and harvest index. These observations were in accordance with earlier workers for plant height (Singh and Singh, 1984), for plant height and seed cotton yield per plant (Singh and Bains, 1968, Dani, 1985, Rajendrakumar *et al.*, 2000, Pushpam *et al.* 2004, Gumber and Chahal, 2006, Gopinath *et al.*, 2009 and Kulkarni *et al.*, 2011). In parental lines, contribution was as follows. Plant height, sympodia per plant, sympodial length at 50 per cent plant height, sympodial angle, seed cotton yield per plant, halo length and ginning out turn contributed to the divergence in that order. The above results implied that in order to select genetically diverse genotypes for hybridization the material should be screened for important traits like plant

height, seed cotton yield per plant, sympodial length at 50 per cent plant height and halo length. The other traits can then be considered based upon the breeding objective.

### Analysis of cluster means

Analysis of cluster means indicated substantial variation among clusters grouped according to D<sup>2</sup> analysis. Based on the range of means it is possible to know the characters influencing divergence. In the genotypes of the present study, Clusters IX, I and VI of F<sub>3</sub> lines and Clusters III and II had higher and lower plant height, respectively. This indicates the wide genetic diversity available in the F<sub>3</sub> lines. The Clusters I, III, IV, V, VII and VIII included lines with less number of sympodial branches and the remaining clusters had lines with more number of sympodial branches per plant. Sympodial length at fifty per cent plant height was higher for Cluster III (59.67) followed by Cluster V (58.97). The remaining clusters had lesser sympodial length at fifty per cent plant height. Genotypes having a lesser sympodial length would occupy lesser radial space in the field which can lead to a higher density planting. Higher productivity can thus be achieved by using such lines to derive genotypes. Interboll distance was more for Cluster V (5.16) and Cluster VI (4.76) whereas, remaining clusters had lesser interboll distance. Numbers of bolls per plant were more in Clusters III, IV and VI and lesser number of bolls were observed in Clusters I, V, IX and VIII which indicated the genetic diversity available in the new F<sub>3</sub> lines.

Boll weight was more in Cluster VIII, V and I, while the remaining clusters had low to moderate boll weight indicating the genetic diversity generated among the F<sub>3</sub> lines. Any hybridization between genotypes of such divergent clusters followed by diligent selection will lead to the accumulation of favorable genes in a selected variety. It was suggested to create variability by involving large number of divergent lines instead of closely related lines by Dani (1985) and Pushpam *et al.* (2004). Ginning outturn was maximum in the Clusters VIII and VII and the remaining clusters had moderate to low ginning outturn. Seed index was observed to be maximum in genotypes of Clusters V. Lint index was more in Clusters VIII, VII and II, whereas, the remaining clusters had moderate lint index. Halo length recorded high values in the genotypes of Cluster IV and IX while the remaining clusters showed medium halo length. This indicated that genetically diverse F<sub>3</sub> lines were residing in these clusters. Seed cotton yield per plant was very high in Clusters VI and IV, and the remaining clusters recorded medium seed cotton yield per plant. This indicates the amount of genetic diversity available in the F<sub>3</sub> lines with respect to seed cotton yield. These results were similar to earlier workers (Singh and Bains, 1968, Dani, 1985, Rajendrakumar *et al.*, 2000, Pushpam *et al.* 2004, Samba Murthy and Chamundeshwari, 2005, Gumber and Chahal, 2006, Gopinath *et al.*, 2009, Satish *et al.*, 2009 and Kulkarni *et al.* 2011) where they noticed seed cotton yield contributed more to genetic divergence.

### Conclusion

Considerable amount of genetic diversity was noticed in the generated material. The contribution of characters indicated that plant height was a major contributor towards divergence

followed by number of nodes per plant, number of seeds per boll and stem girth. The F<sub>3</sub> progeny and parental genotypes were grouped in to 9 and 4 clusters respectively. Cluster I was the largest with 53 and 5 genotypes in both F<sub>3</sub> and parental material, respectively. While Clusters IV, V, VI, VII, VIII, IX in the F<sub>3</sub> set and Cluster IV of the parental set were solitary with one genotype each. The inter cluster D<sup>2</sup> values ranged from 10.16 to 59.15 indicating that considerable amount of diversity existed among the F<sub>3</sub> lines. Therefore, crosses between genotypes of Clusters IV, V, VII, I and IX will generate a wide spectrum of variability for different characters which would help in isolating superior genotypes with improved characters. Similarly, in case of parental lines, crosses between genotypes of Clusters III and IV and will generate good productive hybrids as well as better segregants.

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